

Range : 1 - 1053 Mode : Normal

Codon Table : Universal

5'	9	18	27	36	45	54
ATG	GGC	GAC	CCG	GAA	AGG	CCG
Met	Gly	Asp	Pro	Glu	Arg	Pro
18	27	36	45	54		
GAA	AGG	CCG	GAA	GCG	GCC	GGG
Arg	Pro	Glu	Ala	Ala	Gly	Leu
63	72	81	90	99	108	
TCT	TCA	GAC	ACC	AAC	GAA	AGT
Ser	Ser	Asp	Thr	Asn	Glu	Ser
117	126	135	144	153	162	
AAG	AGT	TCT	CGC	CGG	TTT	GTC
Lys	Ser	Ser	Arg	Arg	Phe	Val
171	180	189	198	207	216	
ATG	TAT	AAA	CAG	GCA	CAG	GCT
Met	Tyr	Lys	Gln	Ala	Gln	Ala
225	234	243	252	261	270	
AAG	GAT	CTC	CCT	CAC	TGG	AAC
Lys	Asp	Leu	Pro	His	Trp	Asn
279	288	297	306	315	324	
CAC	ATC	TTA	GCC	TTT	TTT	GCA
His	Ile	Leu	Ala	Phe	Phe	Ala
333	342	351	360	369	378	
GAG	CGC	TTT	AGT	CAG	GAG	GTG
Glu	Arg	Phe	Ser	Gln	Glu	Val
387	396	405	414	423	432	
CAA	ATT	CTC	ATC	GAG	AAT	GTT
Gln	Ile	Leu	Ile	Glu	Asn	Val

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441	450	459	468	477	486
TAC ATC AGA GAT CCC AAG AAA AGG GAA TTT TTA TTT AAT GCA ATT GAA ACC ATG					
Tyr Ile Arg Asp Pro Lys Lys Arg Glu Phe Leu Phe Asn Ala Ile Glu Thr Met					

495	504	513	522	531	540
CCC TAT GTT AAG AAA AAA GCA GAT TGG GCC TTG CGA TGG ATA GCA GAT AGA AAA					
Pro Tyr Val Lys Lys Lys Ala Asp Trp Ala Leu Arg Trp Ile Ala Asp Arg Lys					

549	558	567	576	585	594
TCT ACT TTT GGG GAA AGA GTG GTG GCC TTT GCT GCT GTA GAA GGA GTT TTC TTC					
Ser Thr Phe Gly Glu Arg Val Val Ala Phe Ala Ala Val Glu Gly Val Phe Phe					

603	612	621	630	639	648
TCA GGA TCT TTT GCT GCT ATA TTC TGG CTA AAG AAG AGA GGT CTT ATG CCA GGA					
Ser Gly Ser Phe Ala Ala Ile Phe Trp Leu Lys Lys Arg Gly Leu Met Pro Gly					

657	666	675	684	693	702
CTC ACT TTT TCC AAT GAA CTC ATC AGC AGA GAT GAA GGA CTT CAC TGT GAC TTT					
Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu His Cys Asp Phe					

711	720	729	738	747	756
GCT TGC CTG ATG TTC CAA TAC TTA GTA AAT AAG CCT TCA GAA GAA AGG GTC AGG					
Ala Cys Leu Met Phe Gln Tyr Leu Val Asn Lys Pro Ser Glu Glu Arg Val Arg					

765	774	783	792	801	810
GAG ATC ATT GTT GAT GCT GTC AAA ATT GAG CAG GAG TTT TTA ACA GAA GCC TTG					
Glu Ile Ile Val Asp Ala Val Lys Ile Glu Gln Glu Phe Leu Thr Glu Ala Leu					

819	828	837	846	855	864
CCA GTT GGC CTC ATT GGA ATG AAT TGC ATT TTG ATG AAA CAG TAC ATT GAG TTT					
Pro Val Gly Leu Ile Gly Met Asn Cys Ile Leu Met Lys Gln Tyr Ile Glu Phe					

873	882	891	900	909	918
GTA GCT GAC AGA TTA CTT GTG GAA CTT GGA TTC TCA AAG GTT TTT CAG GCA GAA					
Val Ala Asp Arg Leu Leu Val Glu Leu Gly Phe Ser Lys Val Phe Gln Ala Glu					

FIG. 2

927	936	945	954	963	972												
AAT	CCT	TTT	GAT	TTT	ATG	GAA	AAC	ATT	TCT	TTA	GAA	GGA	AAA	ACA	AAT	TTC	TTT

Asn	Pro	Phe	Asp	Phe	Met	Glu	Asn	Ile	Ser	Leu	Glu	Gly	Lys	Thr	Asn	Phe	Phe

981	990	999	1008	1017	1026												
GAG	AAA	CGA	GTT	TCA	GAG	TAT	CAG	CGT	TTT	GCA	GTT	ATG	GCA	GAA	ACC	ACA	GAT

Glu	Lys	Arg	Val	Ser	Glu	Tyr	Gln	Arg	Phe	Ala	Val	Met	Ala	Glu	Thr	Thr	Asp

1035	1044	1053							
AAC	GTC	TTC	ACC	TTG	GAT	GCA	GAT	TTT	3'

Asn	Val	Phe	Thr	Leu	Asp	Ala	Asp	Phe	

FIG. 3

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1 (1>351)	Seq2 (1>389)	Similarity
Tp53r2h. pro	R2. pro	Index
(15>351)	(53>389)	80.4
(1>351)	(39>389)	77.5

	10	20	30	40	50	60	70	80																																																																							
TP53R2H	M	G	D	P	E	P	E	A	A	G	L	Q	D	E	R	S	S	S	D	T	N	E	S	E	I	K	S	N	E	E	P	L	L	R	K	S	S	R	R	F	V	I	F	P	I	Q	Y	P	D	I	W	K	M	Y	K	Q	A	Q	A	S	F	W	T	A	E	E	V	D	L	S	K	D	L	P	H	W	N	K	
R2	G	T	R	V	L	A	S	K	T	A	R	R	I	F	Q	E	P	T	E	P	K	T	A	A	A	P	G	V	E	D	E	P	L	L	R	E	N	P	R	R	F	V	I	F	P	I	E	Y	H	D	I	W	Q	M	Y	K	K	A	E	A	S	F	W	T	A	E	E	V	D	L	S	K	D	I	Q	H	W	E	S
	40	50	60	70	80	90	100	110																																																																							

	90	100	110	120	130	140	150	160																																																																							
TP53R2H	L	K	A	D	E	K	Y	F	I	S	H	I	L	A	F	F	A	A	S	D	G	I	V	N	E	N	L	V	E	R	F	S	Q	E	V	Q	V	P	E	A	R	C	F	Y	G	F	Q	I	L	I	E	N	V	H	S	E	N	Y	S	L	L	I	D	T	Y	I	R	D	P	K	K	R	E	F	L	N	A	I	E
R2	L	K	P	E	E	R	Y	F	I	S	H	V	L	A	F	F	A	A	S	D	G	I	V	N	E	N	L	V	E	R	F	S	Q	E	V	Q	I	T	E	A	R	C	F	Y	G	F	Q	I	A	M	E	N	I	H	S	E	N	Y	S	L	L	I	D	T	Y	I	K	D	P	K	R	E	F	L	N	A	I	E	
	120	130	140	150	160	170	180	190																																																																							

	170	180	190	200	210	220	230	240																																																																							
TP53R2H	T	M	P	Y	V	K	K	K	A	D	W	A	L	R	W	I	A	D	R	K	S	T	F	G	E	R	V	V	A	F	A	A	E	G	V	F	F	S	G	S	F	A	A	I	F	W	L	K	K	R	G	L	M	P	G	L	T	F	S	N	E	L	I	S	R	D	E	G	L	H	C	D	F	A	C	L	M	F	Q
R2	T	M	P	C	V	K	K	K	A	D	W	A	L	R	W	I	G	D	K	E	A	T	Y	G	E	R	V	V	A	F	A	A	E	G	I	F	F	S	G	S	F	A	S	I	F	W	L	K	K	R	G	L	M	P	G	L	T	F	S	N	E	L	I	S	R	D	E	G	L	H	C	D	F	A	C	L	M	F	K
	200	210	220	230	240	250	260	270																																																																							

	250	260	270	280	290	300	310	320																																																																								
TP53R2H	Y	L	V	N	K	P	S	E	E	R	V	R	E	I	I	V	D	A	V	K	I	E	Q	E	F	L	T	E	A	L	P	V	G	L	I	G	M	N	C	I	L	M	K	Q	Y	I	E	F	V	A	D	R	L	L	V	E	L	G	F	S	K	V	F	Q	A	E	N	P	F	D	F	M	E	N	I	S	L	E	G	K
R2	H	L	V	H	K	P	S	E	E	R	V	R	E	I	I	N	A	V	R	I	E	Q	E	F	L	T	E	A	L	P	V	K	L	I	G	M	N	C	T	L	M	K	Q	Y	I	E	F	V	A	D	R	L	M	L	E	L	G	F	S	K	V	F	R	V	E	N	P	F	D	F	M	E	N	I	S	L	E	G	K	
	280	290	300	310	320	330	340	350																																																																								

	330	340	350																												
TP53R2H	T	N	F	F	E	K	R	V	S	E	Y	Q	R	F	A	V	M	A	E	T	T	O	N	V	F	T	L	D	A	D	F
R2	T	N	F	F	E	K	R	V	G	E	Y	Q	R	M	G	V	M	S	S	P	T	E	N	S	F	T	L	D	A	D	F
	360	370	380																												

FIG. 4

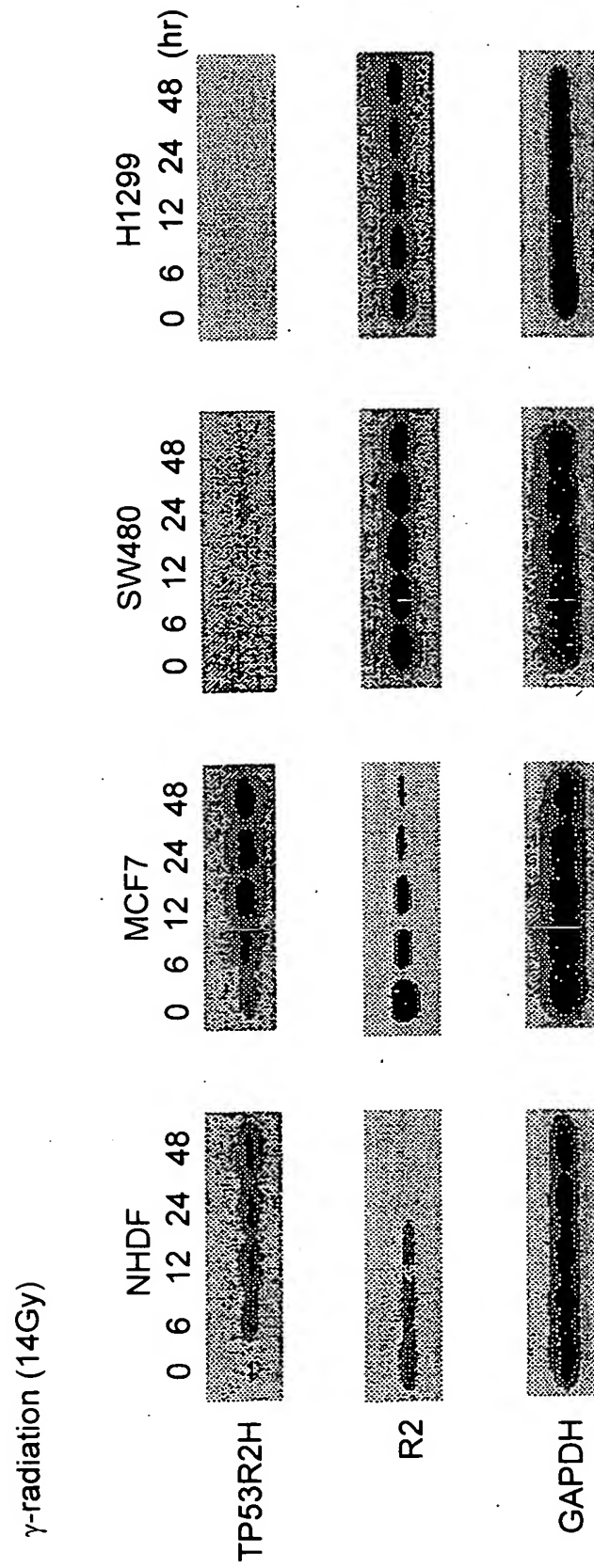


FIG. 5

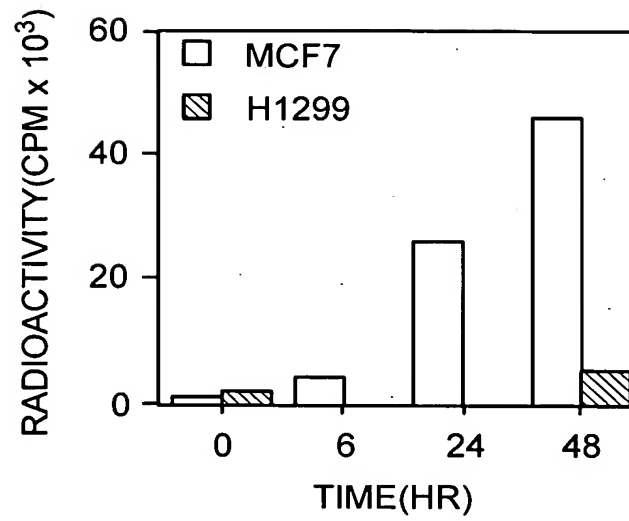


FIG. 6

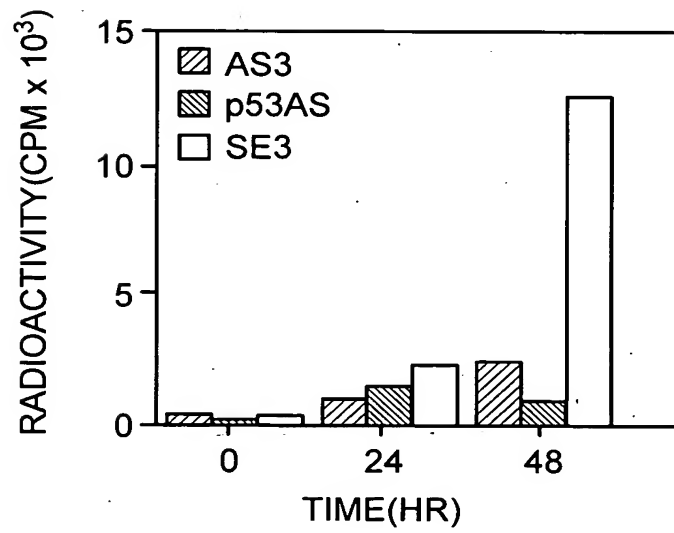


FIG. 7

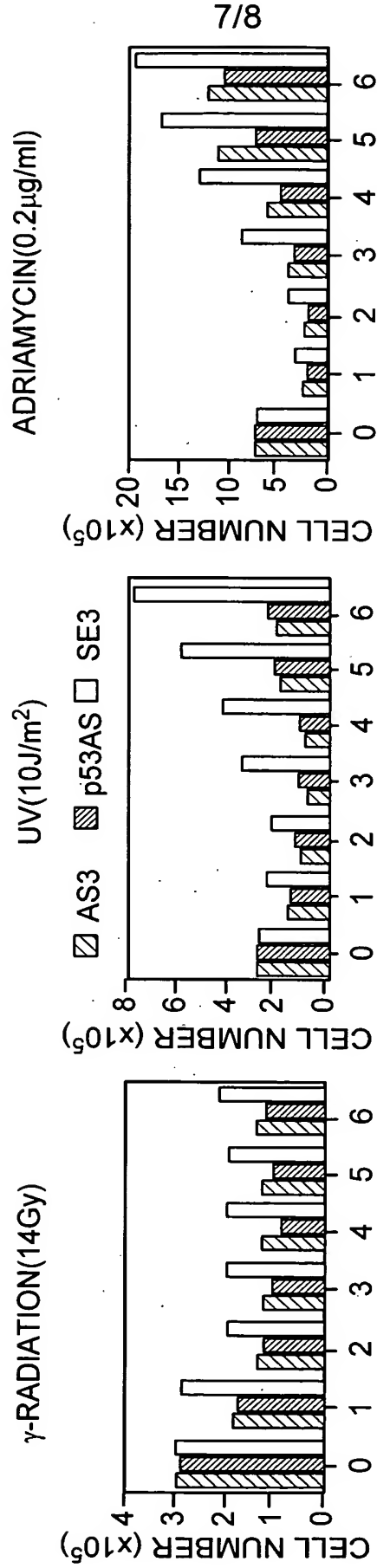
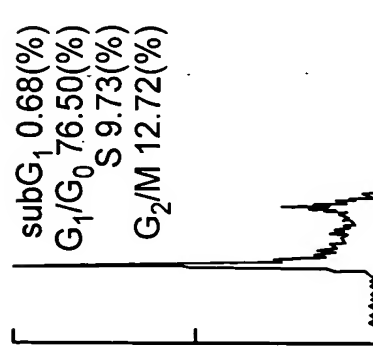


FIG. 8C

FIG. 8B

FIG. 8A

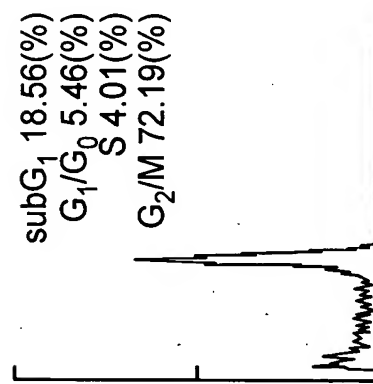
TP53R2H



ADRIAMYCIN(0HR)

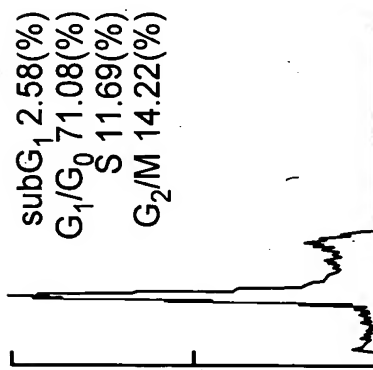
FIG. 9A

pcDNA3.1(+)



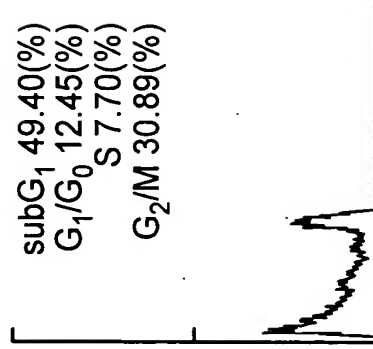
ADRIAMYCIN(48HR)

FIG. 9B



ADRIAMYCIN(0HR)

FIG. 9C



ADRIAMYCIN(48HR)

FIG. 9D

CELLS